EXHIBIT 2

REDACTED IN ITS ENTIRETY

EXHIBIT 3

IN THE UNITED STATES DISTRICT COURT
FOR THE DISTRICT OF DELAWARE

AFFYMETRIX, INC., Plaintiff	)	C.A. No. 04-901 (JJF)
v.	)	
ILLUMINA, INC., Defendant	)	

DECLARATION OF DR. HUBERT KÖSTER

I, Hubert Köster, declare as follows:

1. I am the Managing Director of caprotec GmbH in Berlin, Germany, which succeeded HK Pharmaceuticals, Inc., San Diego, CA. I am the founder and was the Chairman, and CEO of HK Pharmaceuticals, a company providing a novel protein analysis technology allowing the possibility of re-engineering drugs to reduce or eliminate toxic side-effects.

2. I obtained my Vordiplom (equivalent to a Bachelors) in Chemistry in 1963 and my Diplomchemiker (equivalent to a Masters) in Chemistry in 1966, both from the University of Hamburg, in Hamburg, Germany. In 1968, I obtained my Doctorate from the Technical University in Braunschweig, Germany based on work performed at the Max-Planck-Institute in Göttingen, Germany. I later became an Assistant Professor at the University of Hamburg in 1969, and became a tenured Professor in 1982 for Organic Chemistry and Biochemistry. I initiated the formation of Germany's first biotech company in 1981, Biosyntech, and have founded or co-founded a total of four biotech companies, primarily around my own inventions.

3. I am very familiar with the fields of biochemistry and genomics, the latter involving the study of gene and protein expression on the level of the entire genome (an organism's complete genetic blueprint.) I am also familiar with the application of sophisticated

automated instrumentation for the synthesis and analysis of nucleic acids and proteins. At Biosyntech, we developed devices and methods to chemically synthesize DNA that became the standard for the industry and remain the state-of-the-art today. I later served as President and CEO of Sequenom, Inc., presiding over the successful development and commercialization of MassARRAY technology a high-throughput technology designed to analyze single nucleotide polymorphisms ("SNPs,"). I am familiar with microarray technology.

4. I am the author of more than 120 scientific publications and am a named inventor on more than 60 issued patents.

5. I have been retained by Affymetrix to testify in this case. I am being compensated at my usual rate of $ 420 per hour.

6. I have reviewed a one-page abstract entitled "Miniaturization of Sequencing by Hybridization (SBH): A Novel Method for Genome Sequencing" (the "SBH Abstract"), which I understand was cited in connection with a motion Illumina has filed in the litigation between Affymetrix and Illumina in the District of Delaware.

7. I have also reviewed and am familiar with Affymetrix's U.S. Patent No. 6,646,432 (the "'432 patent") and the claims of that patent. Specifically, I am familiar with claims 2, 5, 8, and 9, which I understand are the subject of Illumina's motion.

8. In my opinion, the SBH Abstract does not disclose all of the elements of claims 2, 5, 8, and 9 of the '432 patent in a manner that would enable one of skill in the art to make any collection of beads covered by those claims or to use them for sequence analysis without undue experimentation. The SBH Abstract presents no proof-of-principle, whatsoever, and significant technological obstacles existed at the time, including for example: (a) the ability to specifically synthesize multiple different oligonucleotide sequences on the same beads along with an

encoding system in such a way as to assign the sequence information to individual beads, (b) the ability to design a detection system to allow one to detect multiple hybridizations to the beads, and (c) the ability to fix beads so as to form a monolayer in a manner that would allow functional decoding of the encoding system.

9. One of skill in the art would have been unable at the time to overcome these or other obstacles without undue experimentation. I am unaware of any implementation of these ideas to this day, over 16 years after the SBH Abstract was supposedly prepared.

I hereby declare under penalty of perjury under the laws of the United States of America that the foregoing is true and correct.

Dr. Hubert Köster

July 28, 2006

EXHIBIT 4

REDACTED IN ITS ENTIRETY

EXHIBIT 5

REDACTED IN ITS ENTIRETY

EXHIBIT 6

REDACTED IN ITS ENTIRETY

EXHIBIT 7

REDACTED IN ITS ENTIRETY

EXHIBIT 8

REDACTED IN ITS ENTIRETY

EXHIBIT 9

August 8, 1990

In response to the DOE Human Genome Coordinating Committees request for an advanced SBH proof-of-concept test, I encouraged R. Crkvenjakov and R. Dramanac to first provide a rough draft of their plans. It arrived by FAX on August 6. To me it appeared the content of "Further control tests of SBH method" was sufficiently detailed to be a source for your first critical suggestions. I therefore requested and received permission from them to forward to you, in the still rough English.

With respect to the definition of the fully matched and mismatched probes (MMP) to be utilized, a program will be given to the provider of the DNA to be sequenced, which will output MMP when the sequence is entered. Chosen probes can then be synthesized and provided for the test.

Crkvenjakov wished me to mention two further points. The blot production and interrogations mentioned in their second paragraph are already being implemented in kind in the Lehrach lab. Their target of a million hybridization bits per day represents a target to be achieved through full automation of the blot production/interrogation methodologies. Secondly, Ross Overbeek (ANL) with Dramanac wish to be sponsors of a DOE Hollander Postdoctoral Fellow, who would work on computational aspects of SBH.

I will be on vacation August 5-10. You may transmit your criticisms directly to Crkvenjakov.

Alternatively, I will be happy to serve further as relay point and somewhat cultural translator.

Sincerely yours,

Marvin Stodolsky

Marvin Stodolsky

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" " 5051 facsimile

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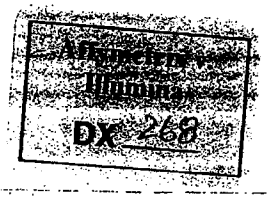


EXPERIMENTAL DESIGN AND METHODS

Our experimental plan is divided into three periods each covering one year.

In the first one, as in most six-month projects, we intend to concentrate on further feasibility tests of SBH. The main one is the reliability of hybridization on unknown DNA. The secondary is the computer testing on simulated data on informatically exceptionally difficult sequences.

Also in the first budget period we intend to assemble the equipment for the production line for hybridization data gathering and optimize the performance of its constituent components. Those are the storage and growth of M 13 clones in individual wells in batches of 1000 microliter plates; the robotic spotting of more than 50,000 clones per 20 x 20 cm membrane, semi-manual hybridization and reading of at least 20 filters per day and others. The daily production capacity will be confirmed at the level of at least one million hybridization data bits. The cDNA and single chromosome libraries will be prepared if not available through collaboration.

In the second budget period for the miniaturization part, the first priority is development of hybridization conditions for the case when oligomer is attached to a bead and fragmented DNA is fluorescently end labeled. Various chemistries of attachment of oligomers to bead and beads to surface will be explored and the optimal chosen.

Also in the second year, the bottlenecks in production line will be addressed and resolved to achieve maximal capacity of one million data bits per day and throughput of at least 2-3,000,000 per day. The number of picked clones in microliter wells will increase to 5-800,000 and definitive biological sequencing experiments will be finalized in the terms of the required kinds and numbers of clones and probes, including the data collected up to this point. During the second period, the preparation of those clones and probes will be completed.

Model microbead surfaces will be prepared and the microscopic automated equipment able to efficiently collect data from these models constructed. Both ordered array and our random, decoded array surfaces will be used. The mixed synthesis of specific oligomers on beads will be explored alone or in collaboration with aim to produce several thousands different oligomers for these experiments.

In the third period, the partial sequencing experiment will be going at a steady data gathering rate of at least a million data bits per day. The necessary improvements in personnel placement and procedures and equipment will be introduced to assure that this performance is no less than the 80% of the maximal rate. Also, the first sequencing chips containing oligomer collections of 10-100,000 oligomers will be prepared according to technologies developed in the first two periods. The pilot data collecting effort with these will be conducted.

In the first period, the intensive effort will go in developing partial SBH algorithms and software able to find sequences from simulated data via

homology and/or motifs in sequence databases. These results are necessary for the fine-tuning of data collecting experiment in terms of kinds and numbers of probes and clones required. If successful, this represents, by itself, an original line of computer research.

Also beginning in the first period, but with main emphasis in the second period, a major effort will be undertaken to set up a database able to efficiently store and provide access of 10^9 data bits. Without this capacity in place, the large data collection would be useless.

In the third period, the integration of the two lines of computer science research will be merged in order to extract biological information on kinds and locations of genes and expressed gene parts from the collected data. It will involve intensive computation. Collaborations will be sought for all aspects of computer research in order to achieve the most efficient data collection. If they are not available, the data collection will have to go hand in hand with the parallel development of computing capabilities.

Experimental Plan

Further control tests of SBH method

These control tests can be divided into biochemical and informatical ones. The biochemical tests serve to measure exactly the hybridization error for specific types of target sequences. For instance, palindromic sequences, regions rich in GC, certain naturally occurring repetitive sequences (i.e., having the high number of mismatched targets), etc., can be chosen for study. The final experimental test is the successful determining of unknown sequence. The problem of such straightforward tests is in the necessity to use the majority of sequence variants for one probe length for sequencing a single clone. For testing 7 to 8 mers which are informatically the most convenient (with the exception of "Sequencing Chip") one needs at least 30,000 probes. Thus, this test must be replaced with the ones that will measure the same thing with much less effort. For example, the sequence can be unknown to the experimenter, but for which a relatively small collection of probes is prepared consisting of all contained in the DNA fragment and, in addition, an appropriate number of probes which should not hybridize with full match in the chosen DNA. Important caveat is that this set of probes should be composed in such a way to prevent its informatical subdivision into predicted positive probes and the others.

The informatical tests would consist of showing the informatical possibilities and limitations in regeneration of the specific types of sequences with set parameters such as numbers and types of probes, numbers and types of clones, magnitudes and types of hybridization data errors. These sequences would represent the extremes of GC content, simplicity and repetitiveness. The general feature of proposed both biochemical and informatical tests is not to extend the theoretical limitations of SBH (,) but to prove the performance of the method within these limits.

The present results show that the hybridization error in experiments with the small number of clones is considerably below the one tolerated by the

algorithm developed for SBH. We propose to repeat the experiment with the maximum of 200 probes on the DNA fragment unknown to experimenter and different from 120 already used, if at all possible. The fragment would be 500-1000 bp long with 70 probes having and 130 probes not having the fully complementary target in it. This would completely mask the situation for experimenter and exclude the subjective bias on hybridization results and final reading of sequence. On the other hand, with additional 200 probes, 1% of all noncomplementary B-mer would be tested removing the fears about the existence of a larger number of specifically nondiscriminative probes. As the result of 100 bp experiment has shown, it is more likely that a certain percent of probes will give unreliable hybridization data which will be recognized by the use of positive controls. The testing of groups of longer probes having these as a core and stabilizing modifications will be used to obtain better results with these probes. The existence of unreliable probes present no problem for partial sequencing, since a portion of total probes is anyway used. At worst, it can impose the need to increase the number of probes by 10%.

Using the phage and cosmid clones of known sequence, a subclone library will be made having the dual role. The first is the supply of necessary positive and negative targets for SBH. The same goal can be accomplished by collecting sequenced clones from different laboratories with a disadvantage of necessity of subcloning of these not presently in M13 vector. The second role of known sequence collection is investigation of influence of complexity, loop structures and GC regions on efficiency of hybridization. Use of probes which have full matches or a larger number of end and other mismatches will allow the assessment of the influence of "surroundings" on the accuracy of sequencing information.

The last type of biochemical test is more important since it will show the extent of random errors and the overall efficiency of the parallel data gathering on the numerous unknown clones simultaneously. We call it "Chain Sequencing." 400 1kb clones and 16 probes will be employed. The probes will be a group of staggered overlapped probes starting with 7-mer 3'end vector sequence. First 4 octamers will be (vect.) A, $(vect.)_7T$, $(vect.)_7C$ and $(vect.)_7G$. and their use will determine the first 5' base in all clones. With further 4 probes of type $(vect.)_6$ an next base pair will be determined in about 100 clones. In next cycle 4 problems of type $(vect.)_5$ AAN will determine 3 bp in about 25 clones. The final cycle with 4 problems $(vect.)_4$ AAAN 4 bp will be determined in about 4-5 clones. The efficiency of the hybridization sequencing will be determined by gel sequencing of a certain number of clones and comparing the actual and SBH predicted sequences. Two types of informatical tests will be done using developed algorithms and software. In the first type the specifically conceived sequences will be presented to the computer. For instance, the theoretical expectation is that an additional group of longer probes with high GC content or 2-3 fold higher representation will be needed for the sequences of more extreme GC content (30%?). The other test will be done on the existing human sequence of 300,000 bp composed from consecutive fragments about 50 kb each. The completeness of regenerated sequence will be tested as a function of used number and types of clones. It is important to stress that there is no theoretical basis for the errors in sequence generation from the errorless data, but just the

ambiguities in connecting shorter correct SFs (i.e., varying degree of completeness). These simulation experiments are tests for the algorithm and can eventually lead to its improvement. All mentioned tests have as their primary goal the recognition and measurement of a certain negative factors affecting SBH. In order to increase the efficiency of SBH by their neutralization they have to be dealt with. The theoretical and experimental results obtained up to now show that the good biochemical and informatical conditions exist for the successful partial and complete SBH. Therefore, it is important to start work on the technological system for partial SBH, the development of components for "Sequencing Chip" and the software package for the efficient analysis of the minimal partial sequence information after a period of a few months of specific control tests or immediately.

SECOND SBH PROOF OF CONCEPT

The SBH team (Crkvenjakov and Drmanac) provided a description of the 2nd stage proof-of-concept tests to be included in their renewal proposal. The tests include extensive testing of their sequence assembly algorithms and interrogation of a 1000 unknown base DNA with some 200 oligomer probes. Both the DNAs and the oligomer probes could be chosen by a DOE designate, with a large number of "hardship" oligomers included. Copies were forwarded to Leroy Hood and Charles Cantor for critiques and subsequent discussion at the August 26th HGCC meeting.

The HGCC recommended that the proposed tests be complemented by a complete SBH sequencing of a ~100 base long DNA, and that this test be so far as possible blind to a knowledge of the sequence. M. Stodolsky suggested that sequence knowledge could be obscured by identifying by codes only, some four target DNAs and the 200 oligomer probes. One of the DNAs should provide data for sequence deduction, while the others would serve as "decoys". The raw data and assembly algorithm software would be provided to the DOE designate for sequence. This suggestion was accepted.

Drmanac telephoned M. Stodolsky on August 29 (Crkvenjakov was traveling) and the scientific content of the recommendations were conveyed. Drmanac found them entirely acceptable and made two points. First there would be little value in having the four DNAs completely unrelated. While one would be sequenced, the rough odds of another DNA yielding positive hybridizations would be roughly 100/70000. But if the DNAs were corresponding segments of DNA from a multi-gene family, the decoys would yield many positive hybridizations as well and interesting examples of their "partial SBH" scheme.

The second point concerned the issue of controls. In the interrogation of any nucleic acid with probes, it is always essential to have positive and negative control DNAs for the probes utilized. Some 100 DNAs ~1000 bases long will eventually be accumulated (such as restriction fragments of lambda and herpes simplex viruses) which together have sequences serving as positive and negative controls for each of the ~70000 oligomer probes to be used in SBH. This is a major future SBH task. But for now, if the identity of the 200 probes is concealed, the DOE designate would also have to provide their negative and positive control DNAs. Drmanac warned that accumulated such control DNAs piecemeal was the most time consuming part of their first proof-of-concept sequencing.

To circumvent the problem of finding a volunteer for task of control DNA collection, Drmanac suggested that the oligomer probes be identified. Then the related DNAs which could not be sequenced would provide abundant cross checks to the DOE designate. The SBH team would gather the control DNAs, as part of their continuing development program.

My personal opinion is that Drmanac's points are usefull and appropriate. There is no reason to doubt their integrity. Others are already using their hybridization methodologies and algorithms. Since the object of SBH is to sequence, achieving blindness is non-trivial. Crkvenjakov has previously stated that any observer/participant was welcome while they were performing their tests. This and independent verification of their procedures are in fact the only proof against any feared "cheating". If cheating was their intention, they could simply sequence their test DNAs by Maxam-Gilbert/Sanger procedures.

EXHIBIT 10

REDACTED IN ITS ENTIRETY

EXHIBIT 11

MINIATURIZATION OF SEQUENCING BY HYBRIDIZATION (SBH): THE "SEQUENCING CHIP" CONCEPT

Drmanac, R. Strezoska, Ž., Labat, I.,
Crkvenjakov, R., Genetic Engineering Center,
P.O. Box 794, 11000 Belgrade, YUGOSLAVIA

IMGGI

Introduction to SBH (Sequencing By Hybridization)

Principle of SBH method is shown in Fig 1. Fig 2 demonstrates that software has been developed that can uniquely reconstruct sequence about 800 bases long from positive oligomer lists. Fig 3 shows that conditions for sequence grade hybridization with octamer probes have been developed for a model array of 54 DNA samples. With these preliminary issues out the way, the poster provides an answer to the question what is the most efficient way of implementing SBH method in genome size sequencing projects.

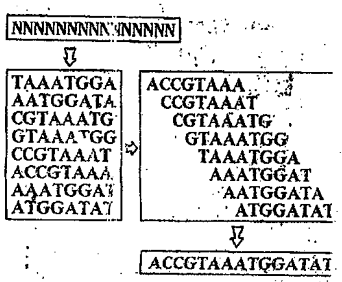
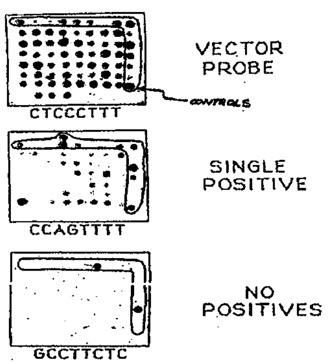


Fig 1
Unknown sequence of 15 nucleotides is determined in 2 steps

1. Biochemical step: Use the hybridization reaction to determine which 8 out of 64000 possible octamer targets exist in the sequence 15 bases long

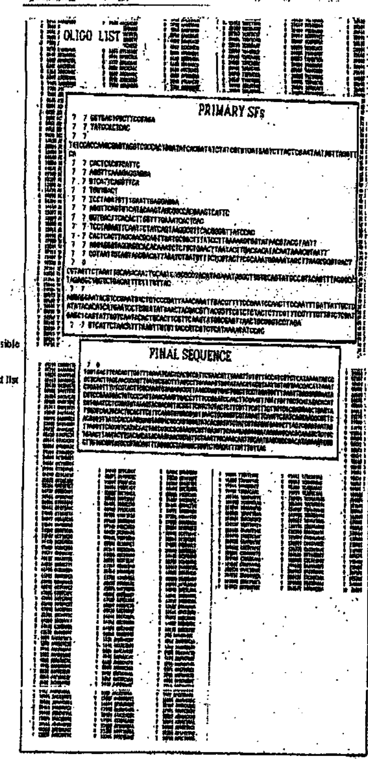
2. Computing step: Order postive octamers in computer using the maximal overlap rule and list the determined sequence



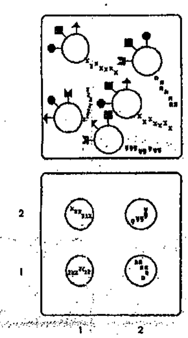
The figure 3 shows fingerprinting of 54 random human cDNA clones in Blue-Script vector with 3 octamer probes. Three situations are illustrated. VECTOR PROBE: All clones hybridize, since probe has the target in Blue-script vector.
SINGLE POSITIVE: Only one of 54 clones has a target sequence in its cDNA insert.
NO POSITIVES: None of the clones has a complementary sequence in the [illegible] The control [illegible] demonstrate efficient hybridization [illegible]

COMPUTING

Computer programs able to uniquely reconstruct sequence from the oligo lists of required completness have been developed. The accompanying poster gives details.



The figure shows original computer listings of input data-oligo list-, intermedite output-unordered short sequence fragments (SFs)-, and final output-correct sequence.



DP CONCEPT AND RECOGNITION PRINCIPLE

FIGURE 1

The figure shows two ways of associating hybridization data obtained from the location on the hybridization surface with a specific clone-probe pair.

i) DP type - association of a physical attributes of DPs like shape, size, color or combination of bound marker oligotargets with a specific clone- probe. The random placement of DPs does not affect the recognition of specific association.

ii) Ordered array type- Placing clone/probe on a predetermined location on hybridization surface, i.e. memorizing both the source address and the location of a clone/probe.

Only principle i) allows miniaturization, i.e. microscale hybridization.

Technological precedents for DP concept

i) The chemistry exists for combinatorial synthesis of oligos on micro beads.

ii) The recently developed fluorescent painting of chromosomes [illegible] the limit of sensitivity [illegible] DNA indicates that DP having size of several [illegible] and chromosomes, one per hybrid [illegible] be easily detected.

OUTLINE OF THE PROPOSED MICROSEQUENCING METHOD BASED ON SEQUENCING BY HYBRIDIZATION (SBH)

1. Bind in the least possible number of reactions, either clones (direct SBH) or all possible oligos of a certain length (inverse SBH) to discrete particles (DPs), basically microbeads of micrometer dimensions without losing the information which sample is bound to which DP.
2. Pour all of them together to form a fixed monolayer hybridisation surface.
3. Recognize under microscope the physical location on the surface of up to 10^9 different DPs, thereby distinguishing as many nucleic acid samples.
4. Hybridize using flourescent label with all possible octamers (65000) in case of Direct SBH, or fragmented genomic DNA of various complexity (individual cosmids, YACs, chromosomes, etc) in case of Inverse SBH.
5. Collect hybridization data by image analysis under fluorescent microscope from 1000 microscope slides (10^4 cm^2 surface).
6. Obtain genomic sequence by computer processing of data.

WHY MICRO-INVERSE SBH ALLOWS THE CONCEPT OF "SEQUENCING CHIP"

From the time and material requirements of direct SBH, the genome project based on this methodology imposes the significant level of robotization (clone preparation and hybridization, particularly if the work is to be performed on small microscope slides), and about one year of work of the average laboratory. The demands of the method are too large for the analysis of more than few genomes, but it is relatively easy to apply experimentally, and is competitive with the existing methods for human genome sequencing. Even more important is the possibility of application of described project for sequencing of the small genomes (up to 10[illegible] bases) and the sequencing of the human, or other, gene (cDNA) sequences.

In the inverse approach, the oligo probes are fixed on the hybridization surface – "Sequencing chip"- and genomic DNA, or mRNA(cDNA), is labeled and serves as a probe. This approach possesses two methodologically very important advantages compared to normal hybridization procedure, and is even more effective if it is possible to apply the number of probes that is larger than the number of clones.

The first advantage is that preparation of the "chip" is independent of sample to be analyzed. That means that "chip" can be prepared beforehand, and the preparation does not affect the speed of the specific experiment. In this way, the share of "chip" costs in the overall project costs is significantly reduced.

The second advantage is the usability in the inverse procedure on the kb scale, thus differing from the direct procedure, which is usable on the mega scale only. This is caused by the compulsory minimal number of probes and hybridizations in direct SBH, which is independent of the length of the analyzed sequence. In the inverse procedure, the number of hybridizations is proportional to the sequence length.

The last advantage described becomes the shortcoming when the inverse procedure is to be applied on the long sequences. For keeping the number of samples (i.e. hybridizations) reasonably small, number of probes to be synthesized and applied to the surface becomes limiting factor. Time and cost difficulties of the macro synthesis of such large number of probes exclude the possibility of the genome project based on the inverse, standard dot hybridization.

Using DP micro hybridization procedure it is possible to avoid macro synthesis of the large number of oligo probes in the large number of separate reactions. In this way, the main difficulty of the application of the inverse procedure in the genome project is eliminated, and its main advantages retained.

THE ESTIMATES OF REQUIREMENTS FOR SEQUENCING HUMAN GENOME

For Direct SBH
- 10^7 clones in microtiter plates, making 10^6 different DPs.
- 10^7 binding reactions (one per well) while memorizing clone-DP association.
- 10 different pools of charged DPs, and formation of 1000 separate hybridization surfaces containing at least 10^7 DPs.
- recognition of specific DP locations by successive hybridizations of all surfaces with 20 longer oligos and imaging.
- hybridization of each surface, either with a different group of 100 differently labeled 8 to 12-mers, or, in a single label case, 100 successive hybridizations of a given surface with a specific oligo from the group and imaging.

For Inverse SBH
- 10^9 different DPs are prepared each carrying: i) one of all possible 15mer oligos, and ii) a specific combination of 20 out of 40 marking oligos. No more than 3000 separate synthesis reactions are needed for their preparation.
- pooling all DPs and spreading in form 100 hybridization surfaces of 10^{10} DPs each.
- recognition of specific locations by successive hybridizations of all surfaces with 40 marker oligos and imaging.
- single hybridization of each surface with mixture of 30 bp fragments of DNA representing specific 1% of human genome (chromosomes, YAC pools, etc.) and imaging.

CREDITS

Direct SBH (bound clones- oligo probes) and the general theory of SBH allowing genomic sequencing
- Drmanac et al. Genomics 4:114 (1989) (first submitted in 1987)

Inverse SBH (bound oligos- clones and probes) for up to 1kb sequences
- Bains and Smith, J. theor. Biol. 135:303 (1988)
- Southern, E., (private communication) (1988)
- Lysov et al. Doklady Acad. Sci U.S.S.R. 303:1508 (1988)

DP concept allowing Microsequencing for both Direct and Inverse SBH
- this work and patents pending.

EXHIBIT 351 DRMANAC 2-21-06